

REMARKS

The above amendments to the above-captioned application along with the following remarks are being submitted as a full and complete response to the Official Action dated August 17, 2004 and the phone interview conducted on October 27, 2004 with the Examiner and her supervisor. Applicants thank the Examiner for taking the time to conduct the interview.

In view of the above amendments and the following remarks, the Examiner is respectfully requested to give due consideration to this application, to indicate the allowability of the claims, and to pass this case to issue.

Status of the Claims

Claims 1-15 are under consideration in this application. Claims 1-6, 8, 10-12 and 14-15 are being amended, as set forth in the above marked-up presentation of the claim amendments, in order to more particularly define and distinctly claim applicants' invention.

Claim Amendments

The claims are being amended to correct formal errors and/or to better recite or describe the features of the present invention as claimed. All the amendments to the claims are supported by the specification.

The method for displaying a dendrogram comprising the steps of: clustering a plurality of biopolymers based on a set of gene expression data (“*displaying data (gene expression data) obtained by hybridization with a specific biopolymer such as a gene*” p. 1, line 4; “*a clustering processor 902 for clustering based on the gene expression patterns*” p. 14, last line) obtained by experiments under different conditions on the plurality of biopolymers, and displaying clustering results thereof in a form of a dendrogram in a display window; selecting a subtree in the dendrogram in the display window; Claim 1: displaying the selected subtree in a separate display window (Fig. 6; p. 7, last paragraph) or Claim 3: replacing the selected subtree with an icon 701 in the dendrogram (Fig. 7; p. 8, 2nd paragraph) thereby simplifying a presentation in the display window (“*by which a global state of the dendrogram can readily be observed*” p. 8, lines 16-17); grouping biopolymers in the selected subtree in the separate display window into at least one function group sharing a common one of functional characteristics including enzymatic (p.2, line 5), metabolic (p. 2, line 6), transporting (Fig. 11), and cell cycle (Fig. 13) functions (“*gene groups with similar*

functions" p. 8, lines 17-18; "*genes belonging to the same cluster may possibly share common functional characteristics*" p. 3, line 7-8; "*function units or function groups are also analyzed by correlating with known enzymatic reaction data or metabolism data*" p. 2, lines 4-6; Function 1104: CELL CYCLE in Fig. 11; Function: TRANSPORT in Fig. 13); and displaying said function group of biopolymers in the separate display window. Claim 2 recites an additional step of designating a different clustering method for said grouping step ("*subtrees of a produced dendrogram can be subjected to different clustering methods interactively*" p. 5, lines 19-20).

The method for displaying a dendrogram of claims 5-6 comprising the same clustering, subtree-selecting, grouping, and function group displaying steps of claims 1 & 3, and the following steps.

Claim 5: selecting keywords from a keyword dictionary file (p. 18, line 20); and counting biopolymers in the subtree whose biopolymer information contains at least one of the selected keywords ("*Figure 8 is a view showing an exemplary screen displayed upon selecting a command 'search for keyword contained in this subtree' from the menu shown in Figure 5. Among genes contained in the selected subtree, genes having gene information with predetermined keywords are counted and the results are displayed as search results 801*" p. 8, last paragraph.) and displaying each of the selected keywords with a corresponding count of the biopolymers whose biopolymer information contains at least one of the selected keywords; displaying the selected keywords and said count in a separated display window on top of the display window displaying said function group of biopolymers therein (Fig. 8) thereby confirming relative biopolymers are assembled in the selected subtree (p. 5, line 20-23; p. 5, lines 1-2).

Claim 6: designating at least one keyword from a keyword dictionary file (p.8, last paragraph; Fig. 8); searching in the selected subtree for biopolymers whose biopolymer information contains the designated keyword; and highlighting in the display window a location of each of the biopolymers in the selected subtree whose biopolymer information contains the designated keyword; displaying the highlighted keywords together with said function group of biopolymers in the display window thereby confirming relative biopolymers are assembled in the selected subtree (Fig. 8).

The biopolymer information includes a unique nucleotide sequence identifier and a description of a corresponding nucleotide sequence, said description includes a source organism, a gene name/protein name, or a function (e.g., "*U25064 Rattus norvegicus*

ubiquitin/60S ribosomal subunit ...” in Fig. 1; “The system is provided with gene data 901 for storing gene information and gene expression patterns” p. 14, last paragraph).

Applicants hereby submit that no new matter is being introduced into the application through the submission of this response.

Formality Rejections

Claims 2, 5 and 10 were objected to for the recitations of “displaying secondarily clustering results” and “information contain one of the predetermined one of the predetermined”. Claims 1-7 and 14 were rejected under 35 U.S.C. § 101 due to the claiming of the non-statutory subject matter. Claims 1-15 were rejected under 35 U.S.C. §112, second paragraph, for being indefinite.

During the interview, the Examiners provided the following comments. First, the proposed amendments introduced new issues which can only be entered via filing an RCE. Second, an outputting or displaying step of the grouped biopolymers needs to be added to all independent claims to overcome the 101 rejection. Third, a linking step should be added into claim 3 between the replacing step and the grouping step, and also into claim 5 between the counting step and grouping step. Fourth, the recitation of “keywords of interest” in claims 5-6 is vague, and the Examiners suggested indicating that the keywords are contained in a file or entered by a user, etc. Fifth, the recitation of “biopolymer information” in claims 5-6 is also vague such that it is unclear what the information includes, i.e., bio-sequences, gene description based upon the GenBank Flat File Format, etc. Lastly, the steps in claim 2 should be amended to better relate back to at least one step of claim 1.

Regarding the claim objections, the claims are being amended as required by the Examiner. Accordingly, the withdrawal of the outstanding claim objections is in order, and is therefore respectfully solicited.

Regarding claims 1-7 and 14 being rejected under 35 U.S.C. § 101 due to the claiming of the non-statutory subject matter. Applicants contend that the recitation of “grouping biopolymers in the selected subtree into at least one function group sharing a common one of functional characteristics including enzymatic, metabolic, transporting, and cell cycle functions is separated as an independent step or means to each independent claim to provide “functional interrelationship as a part of the stored data ... and the process (p.2, last line of the outstanding office action)” and that “displaying said function group of biopolymers in the separate display window” provides a practical application of the invention in the

technological art of gene expression analysis. Applicants contend that such steps or means visually allows one skilled in the art to “*see whether relative genes are assembled in a subtree*” so as to “*determine which function or keyword should be focused on*” (p. 5, lines 1-4). This result “*is concrete, tangible and useful (see AT&T, 172 F.3d at 1358, 50 USPQ2d at 1452)* such that the methods/systems as now claimed are statutory process/system claims (see MPEP 2106 (IV)(b)(ii) Computer-Related Processes Limited to a Practical Application in the Technological Arts). Accordingly, the withdrawal of the outstanding informality rejection is in order, and is therefore respectfully solicited.

The rejections under 35 U.S.C. §112, second paragraph, should be overcome by the method or system for displaying a dendrogram according to the invention, as now recited in the independent claims.

In claims 1, 3, 5, 6 and 8, the step or means for “clustering a plurality of biopolymers based on a set of gene expression data obtained by experiments under different conditions on the plurality of biopolymers” has been specified as based upon gene expression data. As such, it is apparent to one skilled in the art as to the scope of “experiments under different conditions on the plurality of biopolymers” for obtaining the gene expression data. As mentioned, in claims 1, 3, 5, 6 and 8, “grouping biopolymers in the selected subtree into at least one function group sharing a common one of functional characteristics” is now an independent step or means, and the “functional characteristics” are being specified as “including enzymatic (p.2, line 5), metabolic (p. 2, line 6), transporting (Fig. 11), and cell cycle (Fig. 13) functions.” Other functional characteristics known to one skilled in the art include transcription, repair, etc.

Claim 2 is being amended to better relate back to the grouping step of claim 1.

In claim 3, a linking phrase of “simplifying a presentation in the display window” is being added into the step of “replacing the selected subtree with an icon” so as to link to the step of “grouping biopolymers in the simplified presentation in the display window into at least one function group”.

In claim 5, the steps of “displaying said function group of biopolymers in the display window” and “displaying the selected keywords and said count in a separated display window on top of the display window displaying said function group of biopolymers therein thereby confirming relative biopolymers are assembled in the selected subtree” are being added to relate the counting step and grouping step.

In claim 6, new steps of “searching in the selected subtree for biopolymers whose biopolymer information contains the designated keyword” and “displaying the highlighted keywords together with said function group of biopolymers in the display window thereby confirming relative biopolymers are assembled in the selected subtree” are being added to clarify the claim.

In claims 5-6, at least one keyword is selected or designated from a keyword dictionary file, and the “biopolymer information” is being clarified as “includes a unique nucleotide sequence identifier and a description of a corresponding nucleotide sequence, said description includes a source organism, a gene name/protein name, or a function.”

In claims 5 and 12, the counting step is being clarified as “counting biopolymers in the subtree whose biopolymer information contains at least one of the selected keywords and displaying each of the selected keywords with a corresponding count of the biopolymers whose biopolymer information contains at least one of the selected keywords”.

Accordingly, the withdrawal of the outstanding informality rejections is in order, and is therefore respectfully solicited.

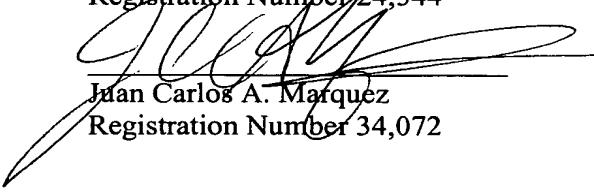
In view of all the above, clear and distinct differences as discussed exist between the present invention as now claimed and the prior art reference upon which the rejections in the Office Action rely, Applicant respectfully contends that the prior art references cannot anticipate the present invention or render the present invention obvious. Rather, the present invention as a whole is distinguishable, and thereby allowable over the prior art.

Favorable reconsideration of this application is respectfully solicited. Should there be any outstanding issues requiring discussion that would further the prosecution and allowance

of the above-captioned application, the Examiner is invited to contact the Applicant's undersigned representative at the address and phone number indicated below.

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